RAW SEQUENCE LISTING DATE: 05/13/2002
PATENT APPLICATION: **US/10/080,114A** TIME: 16:44:40

Input Set : **A:\1301.SEQLIST.TXT**
Output Set: **N:\CRF3\05132002\J080114A.raw**


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 7 <110> APPLICANT: Dhugga, Kanwarpal S.
13 <120> TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
15       to Improve Stalk and Grain Quality
21 <130> FILE REFERENCE: 1301P
25 <140> CURRENT APPLICATION NUMBER: US 10/080,114A
C--> 27 <141> CURRENT FILING DATE: 2002-04-30
31 <150> PRIOR APPLICATION NUMBER: US 60/270,777
33 <151> PRIOR FILING DATE: 2001-02-22
37 <160> NUMBER OF SEQ ID NOS: 13
41 <170> SOFTWARE: FastSEQ for Windows Version 4.0
45 <210> SEQ ID NO: 1
47 <211> LENGTH: 2737
49 <212> TYPE: DNA
51 <213> ORGANISM: Zea mays
55 <400> SEQUENCE: 1
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58 cgtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atcctgcagc cgcaccacat     120
59 cctcgacgcg ctcgacgagg tccagggctc cgggggccgc gcgctagccg agggaccctt     180
60 cctcgacgtc ctccgctccg cgcaggaggc gatcgtgctg ccgccgttcg tggccatcgc     240
61 ggtgcgcccg cgcccgggag tttgggagta cgtccgcgtc aacgttcacg agctcagcgt     300
62 cgagcagctc acagtctcgg agtacctccg cttcaaggag gagcttgtcg acggccagca     360
63 caatgatccc tacgttctcg agcttgactt cgagccgttc aatgtctcag tcccacgccc     420
64 aaatcggtca tcatctattg gaaacggtgt gcagttcctc aaccgacact tgtcctcaat     480
65 catgttccgc aacagggatt gcttggagcc cctgttggat ttcctccgtg gccaccggca     540
66 caaggggcat gttatgatgc ttaatgatag aatacaaagc ttggggaggc ttcagtctgt     600
67 gctgaccaaa gctgaggagc acttgtcaaa gctccctgct gacacaccat actcacaatt     660
68 tgcttataaa tttcaagagt ggggcctgga gaaaggttgg ggtgatacag caggacatgt     720
69 tttggaaatg atccatctcc ttctagacat cattcaggcg ccagacccat ctaccctaga     780
70 gaaattcttg gggaggatcc ccatgatttt taacgttgtt gtggtatccc ctcatggata     840
71 ctttggtcaa gctaatgtat taggcttgcc agacacagga ggacagatcg tctatatact     900
72 ggaccaagtc cgtgcactag aaaatgagat ggttctccgt ttaaagaaac aagggcttga     960
73 tgtttcccca aagattctca ttgttactcg gctgatacca gatgcaaaag gaacatcatg    1020
74 caatcagcgg cttgagagaa ttagtggaac acagcatact tacatattac gagttccctt    1080
75 cagaaatgaa aatgggatac ttaagaaatg gatatcaaga tttgatgtgt ggccatatct    1140
76 ggaaacattt gctgaggatg ctgctggtga aattgctgct gaattacaag gtactccaga    1200
77 cttcataatt ggaaactaca gtgatggaaa tcttgtggcg tcattgctat cttacaagat    1260
78 gggaattacc cagtgcaaca ttgctcatgc tctggaaaag actaagtatc cagattcaga    1320
79 catattttgg aagaatttcg atgagaagta ccatttctcc tgccagttca ctgctgatat    1380
80 aattgctatg aacaatgctg attttatcat caccagcaca taccaagaaa ttgctggaag    1440
81 caaaaatact gttggacagt atgagagtca tactgccttt actctgcctg gtctgtaccg    1500
82 agttgtccat gggatcgatg tcttcgatcc aaagttcaat atagtctctc ctggagctga    1560
83 catgtccata tactttccac ataccgagaa ggccaagcga ctcacctctc ttcatggttc    1620
84 aatcgaaaat ttgatttatg acccggagca aaacgatgaa cacattgggc atctggatga    1680
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PATENT APPLICATION: US/10/080,114A TIME: 16:44:40

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85 ccggtcaaag cccatcctct tctccatggc aagactcgac agggtgaaga acataacagg    1740
86 gctggtcgaa gcttttgcta agtgcgctaa gctgagggag ctggtaaacc ttgtcgtcgt    1800
87 tgccgggtac aatgatgtca acaagtccaa ggacagggaa gagatcgcgg agatagagaa    1860
88 gatgcatgaa ctcatcaaga cccacaactt gttcgggcag ttccgctgga tctctgccca    1920
89 gacaaacagg gcccgtaacg gcgagctcta tcgctacatc gctgataccc atggtgcttt    1980
90 cgtacagccg gccttgtatg aagcgttcgg tctcaccgtc gttgaggcca tgacctgtgg    2040
91 gcttcctact ttcgcgacgc tccatggagg tccagctgag atcatagagc atggcgtctc    2100
92 gggcttccac attgacccgt accaccccga acaggctgtt aatctgatgg ccgacttctt    2160
93 cgaccggtgc aagcaagacc cagatcactg ggtgaatata tctggagcag ggctgcagcg    2220
94 catatacgag aagtacacat ggaagatata ctcagagagg ttgatgacac tggccggggt    2280
95 ctacggtttc tggaagtacg tgtcgaagct cgagaggctg gagacgaggc gctaccttga    2340
96 gatgttctac atactgaagt tccgcgagct ggcgaagacc gtgccgcttg caattgacca    2400
97 accgcagtag cttgcgcaac tgcgactgcg tagcacttgg tacaagactg aaacctgaag    2460
98 gaccttcagt aatttaggcg cggcagacgg tagccaataa aatgtgccgg agctgaactg    2520
99 gtttttttatt atgtacataa tggcagtata acaaaattac tgaaggcagg tgggttgcag    2580
100 ttgtgtgttc gttactgttt actgtattat gtcaagctgt cggctgcaat ttctttgctg    2640
101 gcaagccgca ggcactggtg aagtgctgat aaatacatca tattctgttg acctgtgaaa    2700
102 aaaaaaaaaa aaaaaaaaaa aaaaaaaggg cggccgc                            2737
106 <210> SEQ ID NO: 2
108 <211> LENGTH: 802
110 <212> TYPE: PRT
112 <213> ORGANISM: Zea mays
116 <400> SEQUENCE: 2
118 Ser Thr His Ala Ser Gly Asp Arg Val Glu Asp Thr Leu His Ala His
119  1               5                  10                  15
120 Arg Asn Glu Leu Val Ala Leu Leu Ser Lys Tyr Val Asn Lys Gly Lys
121             20                  25                  30
122 Gly Ile Leu Gln Pro His His Ile Leu Asp Ala Leu Asp Glu Val Gln
123         35                  40                  45
124 Gly Ser Gly Gly Arg Ala Leu Ala Glu Gly Pro Phe Leu Asp Val Leu
125     50                  55                  60
126 Arg Ser Ala Gln Glu Ala Ile Val Leu Pro Pro Phe Val Ala Ile Ala
127 65                  70                  75                  80
128 Val Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val His
129                 85                  90                  95
130 Glu Leu Ser Val Glu Gln Leu Thr Val Ser Glu Tyr Leu Arg Phe Lys
131             100                 105                 110
132 Glu Glu Leu Val Asp Gly Gln His Asn Asp Pro Tyr Val Leu Glu Leu
133         115                 120                 125
134 Asp Phe Glu Pro Phe Asn Val Ser Val Pro Arg Pro Asn Arg Ser Ser
135     130                 135                 140
136 Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Ile
137 145                 150                 155                 160
138 Met Phe Arg Asn Arg Asp Cys Leu Glu Pro Leu Leu Asp Phe Leu Arg
139                 165                 170                 175
140 Gly His Arg His Lys Gly His Val Met Met Leu Asn Asp Arg Ile Gln
141             180                 185                 190
142 Ser Leu Gly Arg Leu Gln Ser Val Leu Thr Lys Ala Glu Glu His Leu
143         195                 200                 205
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PATENT APPLICATION: US/10/080,114A TIME: 16:44:40

Input Set : A:\1301.SEQLIST.TXT
Output Set: N:\CRF3\05132002\J080114A.raw

```
144 Ser Lys Leu Pro Ala Asp Thr Pro Tyr Ser Gln Phe Ala Tyr Lys Phe
145     210                 215                 220
146 Gln Glu Trp Gly Leu Glu Lys Gly Trp Gly Asp Thr Ala Gly His Val
147 225                 230                 235                 240
148 Leu Glu Met Ile His Leu Leu Leu Asp Ile Ile Gln Ala Pro Asp Pro
149                 245                 250                 255
150 Ser Thr Leu Glu Lys Phe Leu Gly Arg Ile Pro Met Ile Phe Asn Val
151             260                 265                 270
152 Val Val Val Ser Pro His Gly Tyr Phe Gly Gln Ala Asn Val Leu Gly
153         275                 280                 285
154 Leu Pro Asp Thr Gly Gly Gln Ile Val Tyr Ile Leu Asp Gln Val Arg
155     290                 295                 300
156 Ala Leu Glu Asn Glu Met Val Leu Arg Leu Lys Lys Gln Gly Leu Asp
157 305                 310                 315                 320
158 Val Ser Pro Lys Ile Leu Ile Val Thr Arg Leu Ile Pro Asp Ala Lys
159                 325                 330                 335
160 Gly Thr Ser Cys Asn Gln Arg Leu Glu Arg Ile Ser Gly Thr Gln His
161             340                 345                 350
162 Thr Tyr Ile Leu Arg Val Pro Phe Arg Asn Glu Asn Gly Ile Leu Lys
163         355                 360                 365
164 Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu Glu Thr Phe Ala
165     370                 375                 380
166 Glu Asp Ala Ala Gly Glu Ile Ala Ala Glu Leu Gln Gly Thr Pro Asp
167 385                 390                 395                 400
168 Phe Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu
169                 405                 410                 415
170 Ser Tyr Lys Met Gly Ile Thr Gln Cys Asn Ile Ala His Ala Leu Glu
171             420                 425                 430
172 Lys Thr Lys Tyr Pro Asp Ser Asp Ile Phe Trp Lys Asn Phe Asp Glu
173         435                 440                 445
174 Lys Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Ile Ile Ala Met Asn
175     450                 455                 460
176 Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser
177 465                 470                 475                 480
178 Lys Asn Thr Val Gly Gln Tyr Glu Ser His Thr Ala Phe Thr Leu Pro
179                 485                 490                 495
180 Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe
181             500                 505                 510
182 Asn Ile Val Ser Pro Gly Ala Asp Met Ser Ile Tyr Phe Pro His Thr
183         515                 520                 525
184 Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu
185     530                 535                 540
186 Ile Tyr Asp Pro Glu Gln Asn Asp Glu His Ile Gly His Leu Asp Asp
187 545                 550                 555                 560
188 Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg Val Lys
189                 565                 570                 575
190 Asn Ile Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg
191             580                 585                 590
192 Glu Leu Val Asn Leu Val Val Val Ala Gly Tyr Asn Asp Val Asn Lys
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RAW SEQUENCE LISTING DATE: 05/13/2002
PATENT APPLICATION: US/10/080,114A TIME: 16:44:40

Input Set : A:\1301.SEQLIST.TXT
Output Set: N:\CRF3\05132002\J080114A.raw

```
193         595                 600                 605
194 Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu
195     610                 615                 620
196 Ile Lys Thr His Asn Leu Phe Gly Gln Phe Arg Trp Ile Ser Ala Gln
197 625                 630                 635                 640
198 Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr
199                 645                 650                 655
200 His Gly Ala Phe Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr
201             660                 665                 670
202 Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His
203         675                 680                 685
204 Gly Gly Pro Ala Glu Ile Ile Glu His Gly Val Ser Gly Phe His Ile
205     690                 695                 700
206 Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe Phe
207 705                 710                 715                 720
208 Asp Arg Cys Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala
209                 725                 730                 735
210 Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile Tyr Ser Glu
211             740                 745                 750
212 Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser
213         755                 760                 765
214 Lys Leu Glu Arg Leu Glu Thr Arg Arg Tyr Leu Glu Met Phe Tyr Ile
215     770                 775                 780
216 Leu Lys Phe Arg Glu Leu Ala Lys Thr Val Pro Leu Ala Ile Asp Gln
217 785                 790                 795                 800
218 Pro Gln
224 <210> SEQ ID NO: 3
226 <211> LENGTH: 36
228 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
236 <223> OTHER INFORMATION: Designed oligonucleotide based upon the adapter
238       sequence and poly T to remove clones which have a
240       poly A tail but no cDNA.
244 <400> SEQUENCE: 3
246 tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa                                  36
250 <210> SEQ ID NO: 4
252 <211> LENGTH: 2746
254 <212> TYPE: DNA
256 <213> ORGANISM: Zea mays
260 <220> FEATURE:
262 <221> NAME/KEY: CDS
264 <222> LOCATION: (72)...(2480)
268 <400> SEQUENCE: 4
270 aaaccctccc tccctcctcc attggactgc ttgctccctg ttgaccattg ggtattctga     60
272 accatcgagc c atg gct gcc aag ctg act cgc ctt cac agt ctt cgc gaa     110
274               Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu
276                1               5                  10
280 cgc ctt ggt gcc acc ttc tcc tcc cat ccc aat gaa ctg ata gca ctc     158
```

RAW SEQUENCE LISTING DATE: 05/13/2002
PATENT APPLICATION: US/10/080,114A TIME: 16:44:40

Input Set : A:\1301.SEQLIST.TXT
Output Set: N:\CRF3\05132002\J080114A.raw

```
282 Arg Leu Gly Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu
284      15                  20                  25
288 ttt tcc agg tat gtt cac cag ggc aag gga atg ctt cag cgc cat cag      206
290 Phe Ser Arg Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln
292  30                  35                  40                  45
296 ctg ctt gcg gag ttt gat gcc ctg ttt gat agt gac aag gag aag tat      254
298 Leu Leu Ala Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr
300                  50                  55                  60
304 gca cca ttt gaa gac att ctt cgt gct gct cag gaa gca att gtg ctc      302
306 Ala Pro Phe Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu
308              65                  70                  75
312 ccc cca tgg gtt gca ctt gct atc agg cca agg cct ggt gtc tgg gat      350
314 Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp
316          80                  85                  90
320 tac att cgg gtg aat gta agt gag ctg gct gtg gag gag ctg agt gtt      398
322 Tyr Ile Arg Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val
324      95                  100                 105
328 tct gag tac ttg gca ttc aag gaa cag ctg gtg gat gga caa tcc aac      446
330 Ser Glu Tyr Leu Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn
332 110                 115                 120                 125
336 agc aac ttt gtg ctt gag ctt gat ttt gag ccc ttc aat gcc tcc ttt      494
338 Ser Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe
340                 130                 135                 140
344 cct cgt cct tcc atg tcg aag tcc atc gga aat gga gtg caa ttc ctt      542
346 Pro Arg Pro Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu
348             145                 150                 155
352 aac cga cac ctg tcg tcc aag ttg ttc cag gac aag gag agt ttg tac      590
354 Asn Arg His Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr
356         160                 165                 170
360 ccc ttg ctg aac ttc ctc aag gct cat aac tac aag ggc acg acg atg      638
362 Pro Leu Leu Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met
364     175                 180                 185
368 atg ttg aat gac aga atc caa agc ctt cgt ggt ctc caa tca tcc ctg      686
370 Met Leu Asn Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ser Leu
372 190                 195                 200                 205
376 aga aag gca gag gag tat cta ctg agt gtt cct caa gac act ccc tac      734
378 Arg Lys Ala Glu Glu Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr
380                 210                 215                 220
384 tcg gag ttc aac cat agg ttc caa gag ctt ggc ttg gag aag ggt tgg      782
386 Ser Glu Phe Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp
388             225                 230                 235
392 ggt gac act gcg aag cgt gtt ctc gac aca ctc cac ttg ctt ctc gac      830
394 Gly Asp Thr Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp
396         240                 245                 250
400 ctt ctt gag gcc cct gat cct gcc aac ttg gag aag ttc ctt gga act      878
402 Leu Leu Glu Ala Pro Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr
404     255                 260                 265
408 ata cca atg atg ttc aac gtt gtt atc ctg tct cct cat ggc tac ttc      926
410 Ile Pro Met Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe
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VERIFICATION SUMMARY DATE: 05/13/2002
PATENT APPLICATION: **US/10/080,114A** TIME: 16:44:41

Input Set : **A:\1301.SEQLIST.TXT**
Output Set: **N:\CRF3\05132002\J080114A.raw**

L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1452 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:1460 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11